IN THE SPECIFICATION

Please amend the specification pursuant to 37 C.F.R. § 1.121 as follows(see the accompanying "marked-up" version pursuant to 1.121):

Replace the first full paragraph on page 4 with the following paragraph:

Figure 1 is a schematic illustration of the oligonucleotides used for PCR amplification of human estrogen receptor-β ($hER\beta_L$) cDNA (SEQ ID NO:5 and SEQ ID NO:6).

Replace the first full paragraph on page 7 with the following paragraph:

Alignment of the known rat ERβ sequence (Kuiper et al., *Proc.Natl.Acad.Sci.USA* **93**:5925, 1996) with that of a human homologue (Mosselman et al., *FEBS Letts.* **392**:49, 1996) suggested that the human sequence lacked at least the ultimate and penultimate residues at its aminoterminus, as shown below:

Rat: MTFYSPAVMNYS . . . (SEQ ID NO:3)

Human: - - GYSPAVMNYS . . . (SEQ ID NO:4)

Based on this information, PCR primers were designed that supplement the human sequence with the two missing aminoterminal residues M and T and with an artificial Kozak translation initiation sequence. The forward primer, having the sequence (SEQ ID NO:5) 5'-GGAAGCTTGTCGACCATCATGACCGGCTATAGCCCTGCTGTGATG-3' and a reverse primer, having the sequence (SEQ ID NO:6) 5'-GGATCTAGAGTCGACGCGTCACTGAGACTGAGGGTTCTGG-3' were used to amplify hERβ sequences in a reaction containing the following components: 2 μl of the cDNA

template described above; 1X PCR buffer; 200 μM of each deoxynucleoside triphosphate, 2 units of hot tab polymerase (Amersham, Arlington Heights IL), and 1μg of each of the forward and reverse primers. The reaction mixture was heated to 95°C for 2 minutes, annealed at 52°C for 1 minute, and amplified using 36 cycles of 72°C for 1.5 minutes.

Replace the first full paragraph on page 8 with the following paragraph:

A fragment of approximately 1500 bp in length was produced. The fragment digested with *Hind*III and *Xba*I (which cleave at sites present in the forward and reverse primer sequences, respectively, but not in the main body of the amplified cDNA sequence) and cloned into the corresponding sites of the pcDNA3 expression vector (Invitrogen, Carlsbad CA). This assymetric cloning strategy places the 5' end of hERβ cDNA under the control of the viral CMV promoter in pcDNA3 (Figures 1 and 2). Several insert-containing pcDNA3 clones were identified. Plasmid DNA was prepared from three clones using a plasmid purification kit (Qiagen, Santa Clarita CA) and their insert sequences were determined by the dideoxy termination method. One clone (designated R61010-2.24 or Clone 3) was found to contain an insert with a nucleotide sequence identical to the published hERβ sequence (Mosselman et al., *FEBS Letts.* **392**:49, 1996) and had the following 5' end structure:

M T G Y . . . (SEQ ID NO:7)
CCATC ATG ACC GGC TAT . . . (SEQ ID NO:8)

This clone was designated "truncated hERβ" or $hER\beta_T$.

Replace the second full paragraph on page 8 with the following

paragraph:

To verify the aminoterminal and upstream sequence of human hERβ, two independent approaches were taken, as described below.

(1) 10 μl of a human ovary 5'-Stretch cDNA library (Clontech, Palo Alto CA) was mixed with 50 μl of 1X K solution (1X PCR Buffer (GIBCO-BRL, Gaithersburg MD), 2.5 mM $MgCl_2$, 0.5% Tween-20, 100 μg/ml Proteinase K), and the reaction mixture was incubated at 56°C for 2 hours, then at 99°C for 10 minutes. 5 μl of this reaction mixture were then used as template in a nested PCR reation. For the first round, the forward primer (pDR2 sequencing primer, Clontech, Palo Alto CA) had the sequence 5'-CTGGTAAGTTTAGTCTTTTTGTC-3' (SEQ ID NO:9), and the reverse primer (hERβ-specific, designated oligo #12908) had the sequence 5'-GCTTCACACCAAGGACTCTTTTGAG-3' (SEQ ID NO:10). The reaction contained 1X Klentaq PCR reaction buffer (40 mM Tricine-KOH, 15 mM KOAc, 3.5 mM $Mg(OAc)_2$, 75 μg/ml bovine serum albumin); 0.2 mM of each dNTP; 0.2 μM of each of the above primers, and 1 unit of Klentaq Polymerase Mix (Clontech, Palo Alto CA). Touchdown PCR conditions were as follows: 5 cycles of 94°C for 2 seconds and 72°C for 4 minutes, followed by 30 cycles of 94°C for 2 seconds and 67°C for 3 minutes.

Replace the first full paragraph on page 9 with the following paragraph:

Excess nucleotides and primers were removed from the first round PCR reactions by purification over Wizard PCR columns (Promega, Madison WI). A second-round PCR reaction was performed using 2 μl of the purified first round reaction

mixture. For the second round, the forward primer was the pDR2 sequencing primer shown above, and the reverse primer had the sequence 5'-GTTGGCCACAACACATTTGGGCTTGT-3' (hERβ-specific, designated oligo #13871) (SEQ ID NO:11). The second round PCR reaction and cycling conditions were identical to those employed in the first round. The products were cloned into the pCR2.1 vector and two clones were sequenced. All three clones (designated L1, L2, and L3) contained hERβ inserts of different lengths, all of which were homologous to hERβ, and to each other.

Replace the second full paragraph on page 9 with the following paragraph:

(2) A Marathon Ready thymus cDNA kit (Clontech) for 5' rapid amplification of cDNA ends (RACE) was also used to isolated hERβ 5' clones. In the first round of a nested PCR reaction, 5 μl of human thymus Marathon-ready cDNA (Clontech) was used as template. The forward primer had the sequence 5'-CCATCCTAATACGACTCACTATAGGGC-3' (Adaptor primer 1, Clontech) (SEQ ID NO:12), and the reverse primer had the sequence 5'-GCTTCACACCAAGGACTCTTTTGAG-3' (hERβ-specific, designated oligo #12908) (SEQ ID NO:10). The PCR reaction and cycling conditions were identical to those described in (1) above.

Replace the first full paragraph on page 10 with the following paragraph:

Excess nucleotides and primers were removed from the first round PCR